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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=4; day=15; hr=13; min=10; sec=12; ms=469; ]

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Application No: 10532681 Version No: 2.0

**Input Set:****Output Set:**

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**Finished:** 2010-04-07 18:29:53.866  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 353 ms  
**Total Warnings:** 22  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 23  
**Actual SeqID Count:** 23

| Error code | Error Description                                   |
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| W 402      | Undefined organism found in <213> in SEQ ID (2)     |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (3)  |
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| W 213      | Artificial or Unknown found in <213> in SEQ ID (5)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (6)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (7)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (8)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (9)  |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (10) |
| W 402      | Undefined organism found in <213> in SEQ ID (11)    |
| W 402      | Undefined organism found in <213> in SEQ ID (12)    |
| W 402      | Undefined organism found in <213> in SEQ ID (13)    |
| W 402      | Undefined organism found in <213> in SEQ ID (14)    |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (15) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (16) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (17) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (18) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (19) |
| W 213      | Artificial or Unknown found in <213> in SEQ ID (20) |

**Input Set:**

**Output Set:**

**Started:** 2010-04-07 18:29:50.513  
**Finished:** 2010-04-07 18:29:53.866  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 353 ms  
**Total Warnings:** 22  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 23  
**Actual SeqID Count:** 23

| Error code | Error Description                                   |
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# SEQUENCE LISTING

<110> LUKYANOV, SERGEY A  
SHAGIN, DMITRY A  
YANUSHEVICH, YURY G

<120> FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA  
HYDROZOA SPECIES AND METHODS FOR USING SAME

<130> U 015745-9

<140> 10532681

<141> 2010-04-07

<160> 23

<170> PatentIn version 3.4

<210> 1

<211> 784

<212> DNA

<213> Phialidium sp.

<400> 1

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ggttatggag atgcaagtgt tggtaaagtt gatgccaat tcatctgcac aactggagat      180
gtaccagttc catggtcaac tttagtaaca acacttactt atggtgcaca atgcttcgcc      240
aaatatggtc cagaattaaa ggatttctac aagagttgca tgctgaagg ctatgtgcag      300
gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctgcgctga agttacattt      360
gaaaacggat ctgtttataa ccgagtcaaa cttaatggac aaggatttaa gaaagacgga      420
catgtgcttg gaaagaatct tgaattcaat ttcacacctc attgtcttta catttgggga      480
gatcaggcta atcatggttt gaagtctgct ttcaaaatta tgcattgagat tactggatca      540
aaagaagact tcattgttgc agaccacacc caaatgaaca caccatttgg tggatggacca      600
gtccatgtcc ctgaatacca tcatataaca taccatgtca ctctcagcaa agatgttact      660
gatcacaggg ataacatgag cttgggtgaa accgtacggg ctgtggattg cagaaaaaca      720
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<212> PRT

<213> Phialidium sp.

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1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 3  
<211> 705  
<212> DNA  
<213> Artificial sequence

<220>  
<223> phiYFP-Y1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180  
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240  
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300  
gacggagtat ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360  
gtcaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa 420  
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag 480  
tctgctttca aaattatgca tgagattact ggatcaaaag gagacttcat tgttgcagac 540  
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600  
atgacatacc atgtcactct cagcaaagat gttactgatc acagggataa catgagcttg 660  
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<210> 4  
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<212> PRT  
<213> Artificial sequence

<220>  
<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 5

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-M0 mutant of the phiYFP

<400> 5

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta    180
gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atgggtccaga attaaaggat    240
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg    300
gacggaaact ttaaaactcg cgetgaagtt acatttgaaa acggatctgt ttataaccga    360
gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa    420
ttcaatttca cacctcattg tctttacatt tggggagatc aggctaata tggtttgaag    480
tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttgcacac    540
cacacccaaa tgaacacacc cattggtggt ggaccagtcc atgtccctga aaaccatcat    600
atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg    660
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<210> 6

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M0 mutant of the phiYFP

<400> 6

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Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
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```
Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20              25              30
```

```
Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35              40              45
```

```
Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50              55              60
```

```
Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
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| 65  | 70  | 75  | 80  |
|---|-----|-----|-----|
| Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile |     |     |     |
|   | 85  | 90  | 95  |
| Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe |     |     |     |
|   | 100 | 105 | 110 |
| Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe |     |     |     |
|   | 115 | 120 | 125 |
| Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr |     |     |     |
|   | 130 | 135 | 140 |
| Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys |     |     |     |
|   | 145 | 150 | 155 |
| Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe |     |     |     |
|   | 165 | 170 | 175 |
| Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro |     |     |     |
|   | 180 | 185 | 190 |
| Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser |     |     |     |
|   | 195 | 200 | 205 |
| Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val |     |     |     |
|   | 210 | 215 | 220 |
| Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu                         |     |     |     |
|   | 225 | 230 |     |

<210> 7

<211> 705

<212> DNA

<213> Artificial sequence

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<223> phiYFP-M1 mutant of the phiYFP

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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180

gtaacaacac ttacttatgg tgcacaatgc ttcgccaaat atggtccaga attaaaggat 240  
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 gacggaaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360  
 gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatcttgaa 420  
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 cacacccaaa tgaacacacc cattgggtggg ggaccagtcc atgtccctga ataccatcat 600  
 atgagctacc atgtcaagct cagcaaagat gttactgatc acagggataa catgagcttg 660  
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<210> 8

<211> 234

<212> PRT

<213> Artificial sequence

<220>

<223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
 1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys  
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

<210> 9

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> humanized version of the phiYFP-M1

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gtgaccaccc tgacctacgg cgcccagtgc ttcgccaagt acggccccga gctgaaggat 240

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gatggcaatt tcaagaccgc cgccgaggtg accttcgaga atggcagcgt gtacaatcgc 360

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<210> 10

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<212> PRT

<213> Artificial sequence

<220>

<223> humanized version of the phiYFP-M1

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val  
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys  
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys  
35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu  
50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp  
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile  
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe  
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe  
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr  
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys

145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe  
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro  
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser  
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val  
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu  
225 230

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<212> DNA  
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<220>  
<221> misc\_feature  
<223> hydromedusa 1 from sub-order Anthomedusae

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ggtgtcaaaa atttacgttc tagaaattgc agtacggaag aaaaaccgt catacttggt 180  
gcaatgacag aacatttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240  
gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tgggtgtaatt 300  
gaaggaaaat atgtttgtac agaaggagaa gtccctatct catgggttcc gctcatcacc 360  
tcattaagtt atggtgcgaa atgttttgtt cgatatccaa atgaaataaa tgattttttc 420  
aaaagtactt ttccttctgg atatcatcaa gaaagaaaaa ttacatatga gaatgatggt 480  
gttttagaaa cagcagctaa aattactatg gaaagtgggt caatagtga tagaataaat 540  
gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc 600  
cctccttcga caacatatgt tgttcccgag ggagaaggta ttcgaatcat ctatagaaac 660  
atctatccaa caaagatgg tcactatggt gttgccgaca cacagcaagt aaatcgacca 720

|  |      |
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| ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca  | 840  |
| tttgacgctg atttttctta agatttcgga tttgcatcaa gattgaaaaa ctaaataaag  | 900  |
| ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa  | 960  |
| tatatatttca aataaacttt ataaaattag gaatctttga atatataaac taaacctttt | 1020 |
| atttgtagaa taaaaataat taaagac                                      | 1047 |

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